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Exposure to Sample

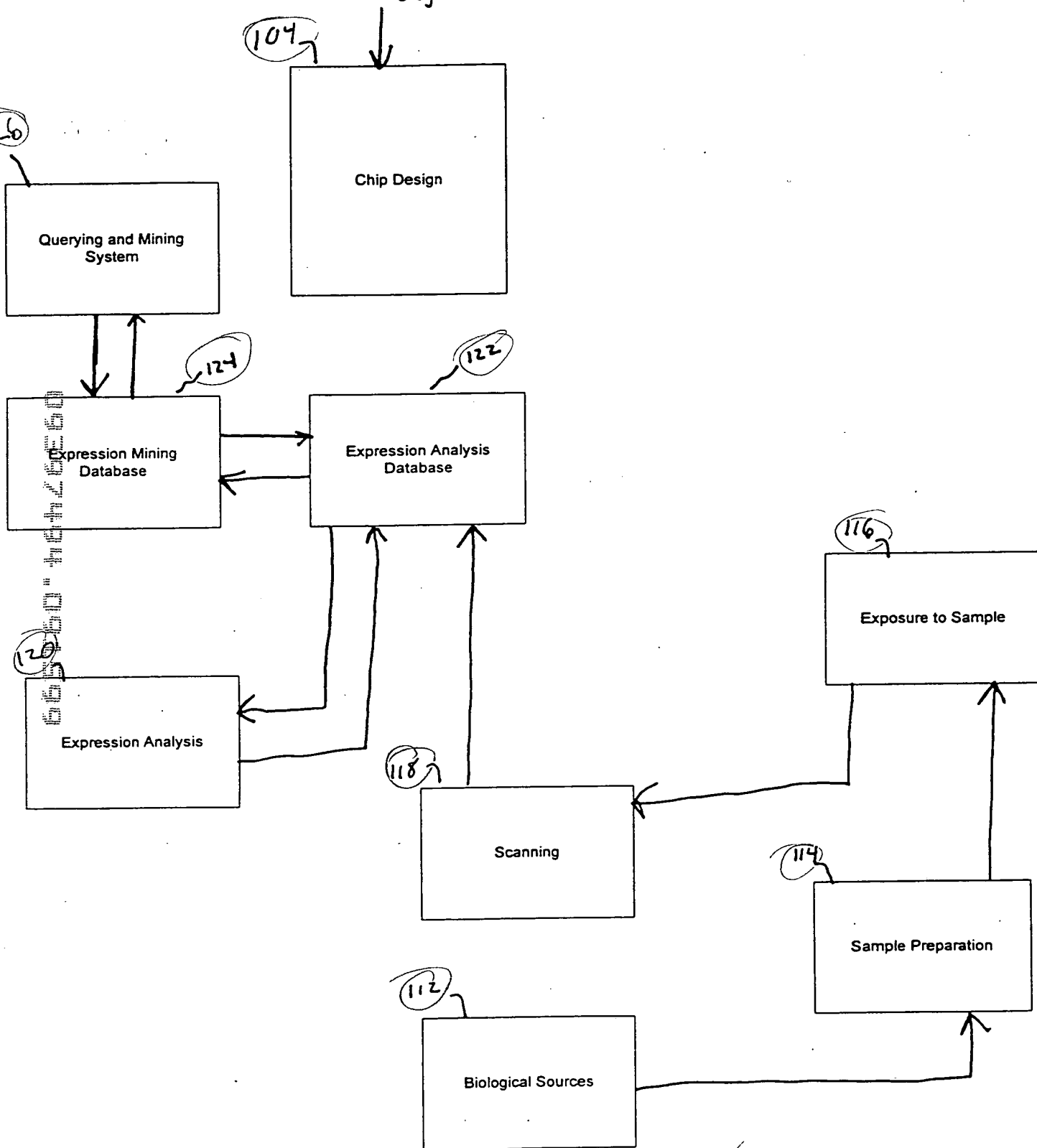
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Sample Preparation

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Biological Sources

Fig. 1



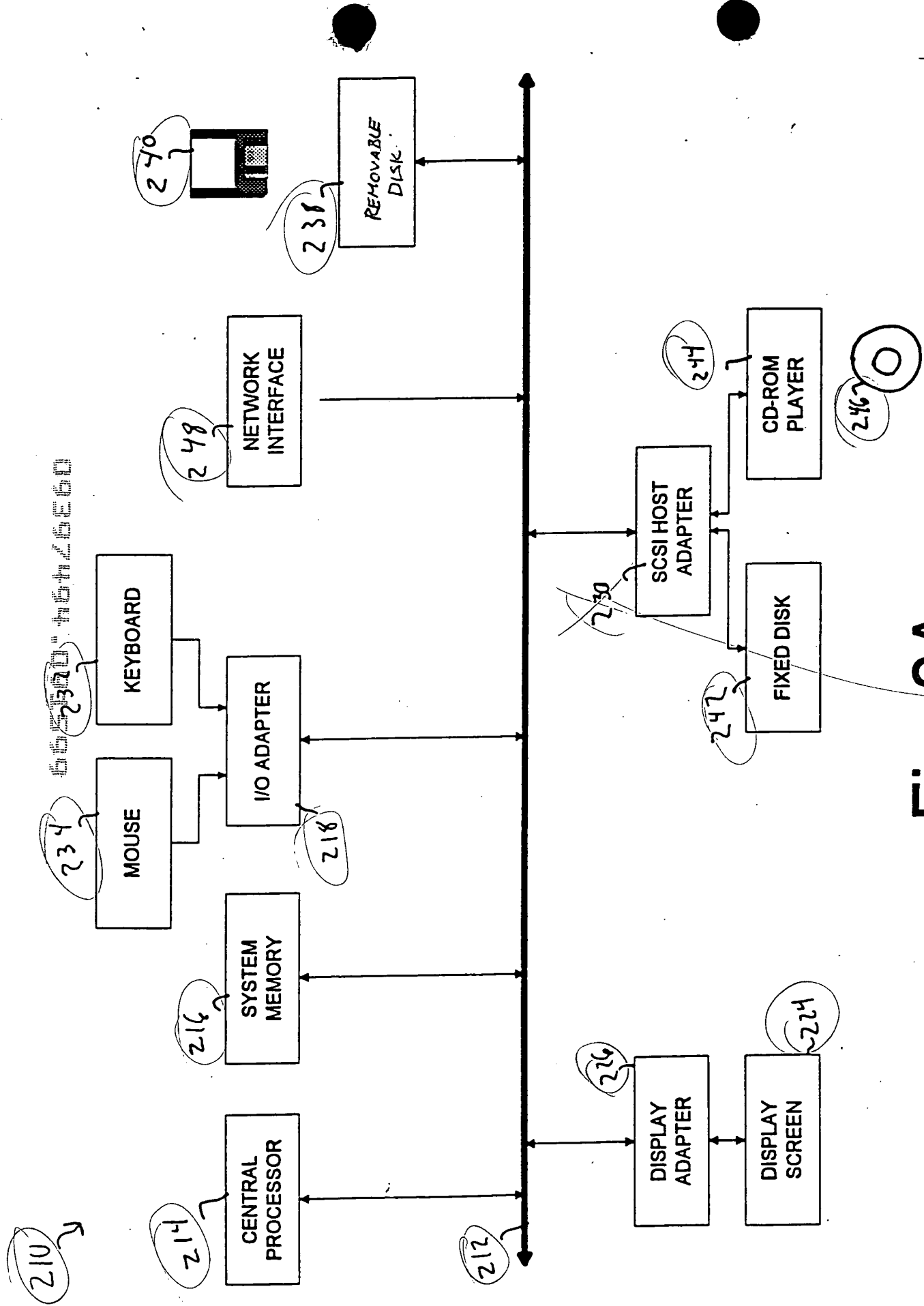


Fig. 2A

665T60"46H26E60

LAN

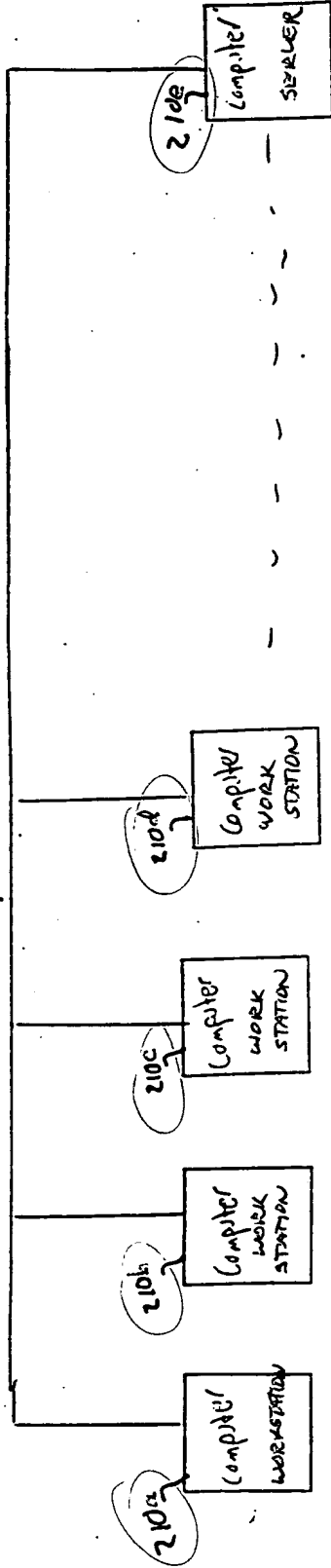


Fig. 2B

655T60" 46426E60

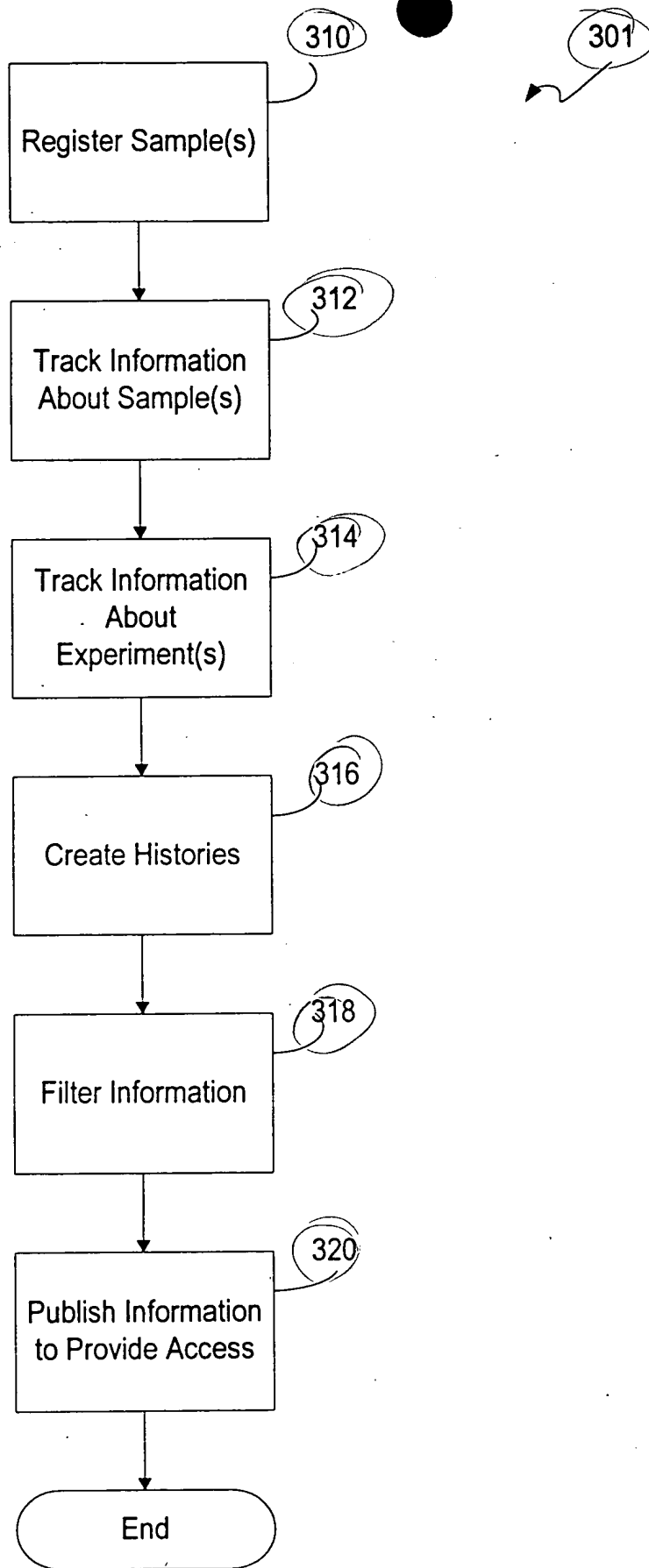


Fig. 3A

665760" 4642660

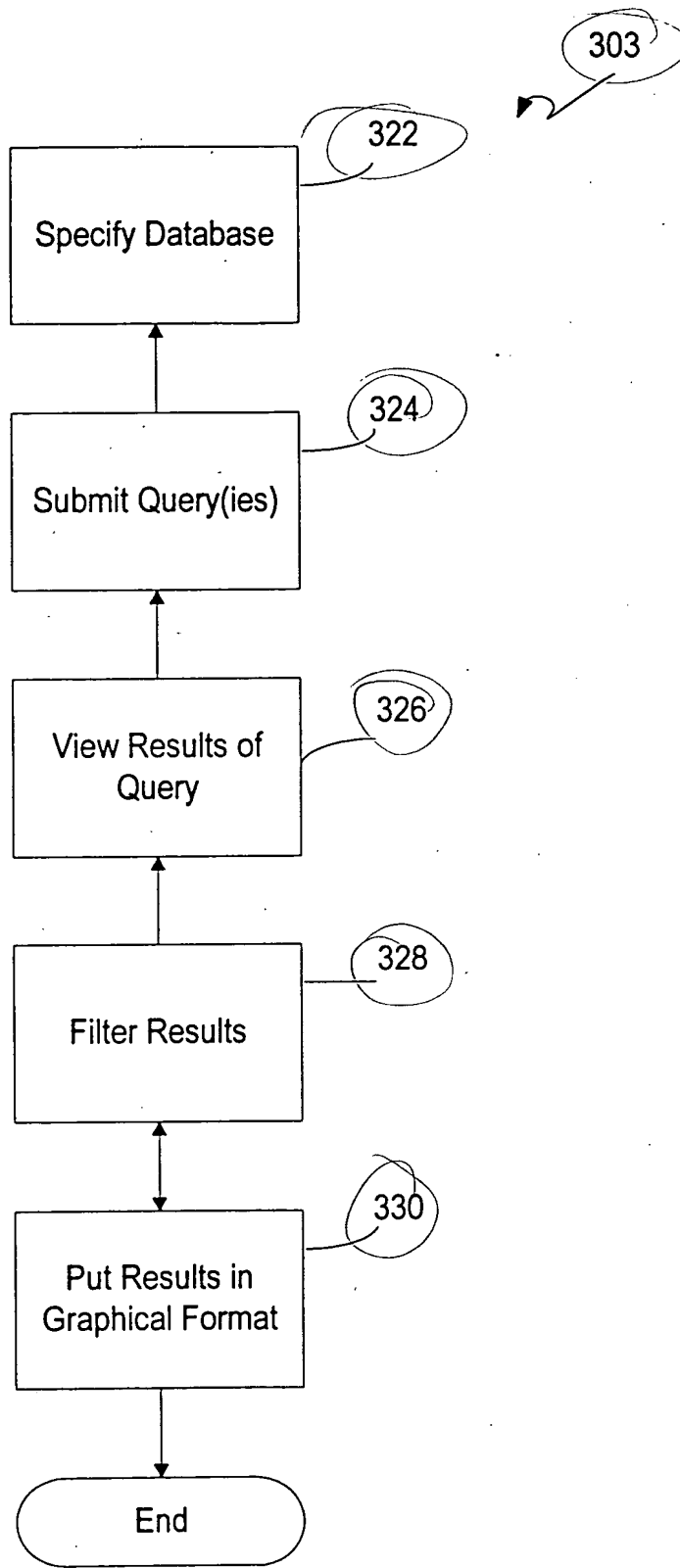


Fig. 3B

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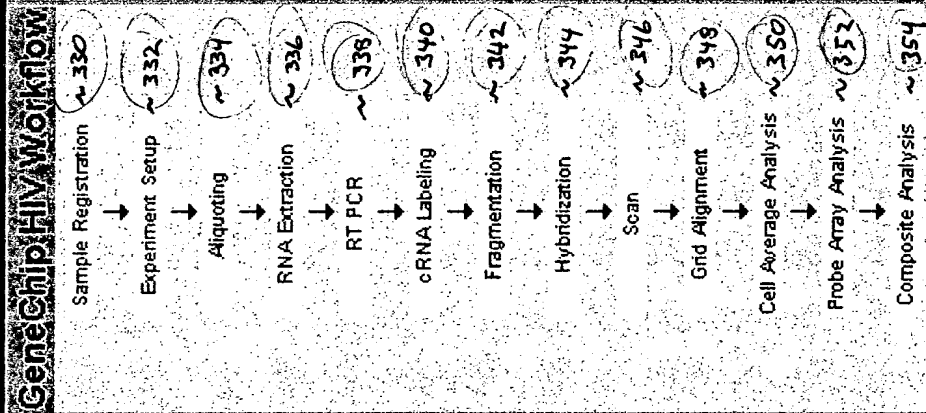


Fig. 30

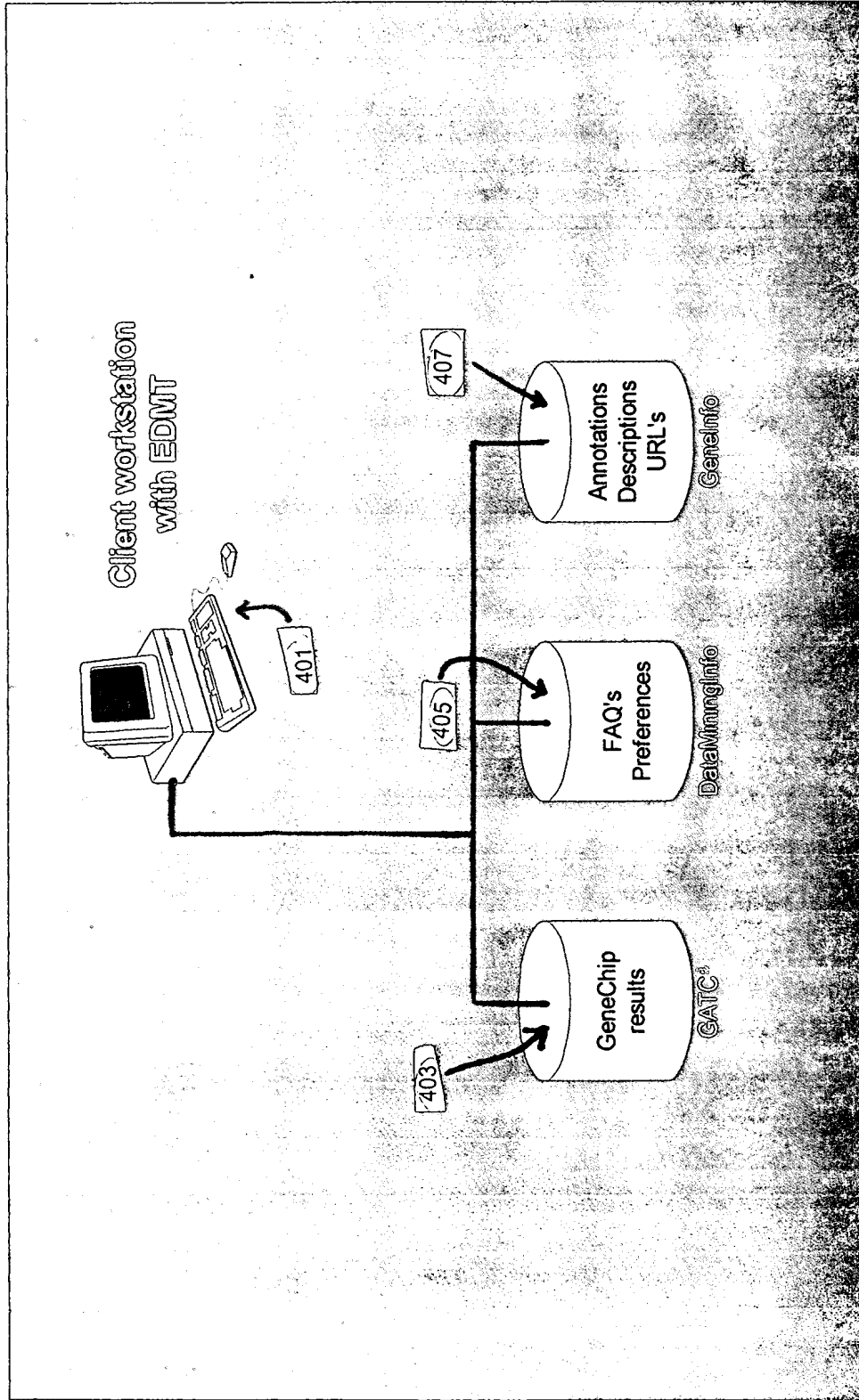


Fig. 4A

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All DSN's on workstation

Currently selected DSN



Fig. 4B

GeneChip Expression Automation

Sample Info:

Sample name:

Sample type:

Sample project:

Description:

Comments:

Experiment Info:

Experiment name:

Probe Array Image ID:

Probe Array Types:

Probe Array Lot #:

Cell Average Set:

Probe Array Analysis Set:

Publish Database:

Automate Clear

Sample/Experiment/Probe array image ID:

Sample	Experiment	Probe array image ID
Demo	DemoEsubA	DemoCsubA
Demo	DemoEsubB	DemoCsubB
Demo	DemoEsubC	DemoCsubC
Demo	DemoEsubD	DemoCsubD
Demo1	Demo1EsubA	Demo1EsubB
Demo1	Demo1EsubC	Demo1EsubD

Multiple experiments per sample

Multiple samples

Use parameter sets

Fig. 5A

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Comments:

Cell Average Set:

Probe Array Analysis Set:

Publish Database:

Automate

Results

Result	Message
Pass	Sample Demo passed registration
Pass	Experiment DemoSubA passed automation
Pass	Sample Demo passed requere
Pass	Experiment DemoSubB passed automation
Pass	Sample Demo passed requere
Pass	Experiment DemoSubC passed automation
Pass	Sample Demo passed requere
Pass	Experiment DemoSubD passed automation
Pass	Sample Another Demo passed registration
Pass	Experiment Another DemoSubA passed automation
Pass	Sample Another Demo passed requere
Pass	Experiment Another DemoSubB passed automation
Pass	Sample Another Demo passed requere
Pass	Experiment Another DemoSubC passed automation
Pass	Sample Another Demo passed requere
Pass	Experiment Another DemoSubD passed automation

First Sample is registered

First Experiment setup

First Sample is re-queued

Second Experiment setup

Fig. 5B

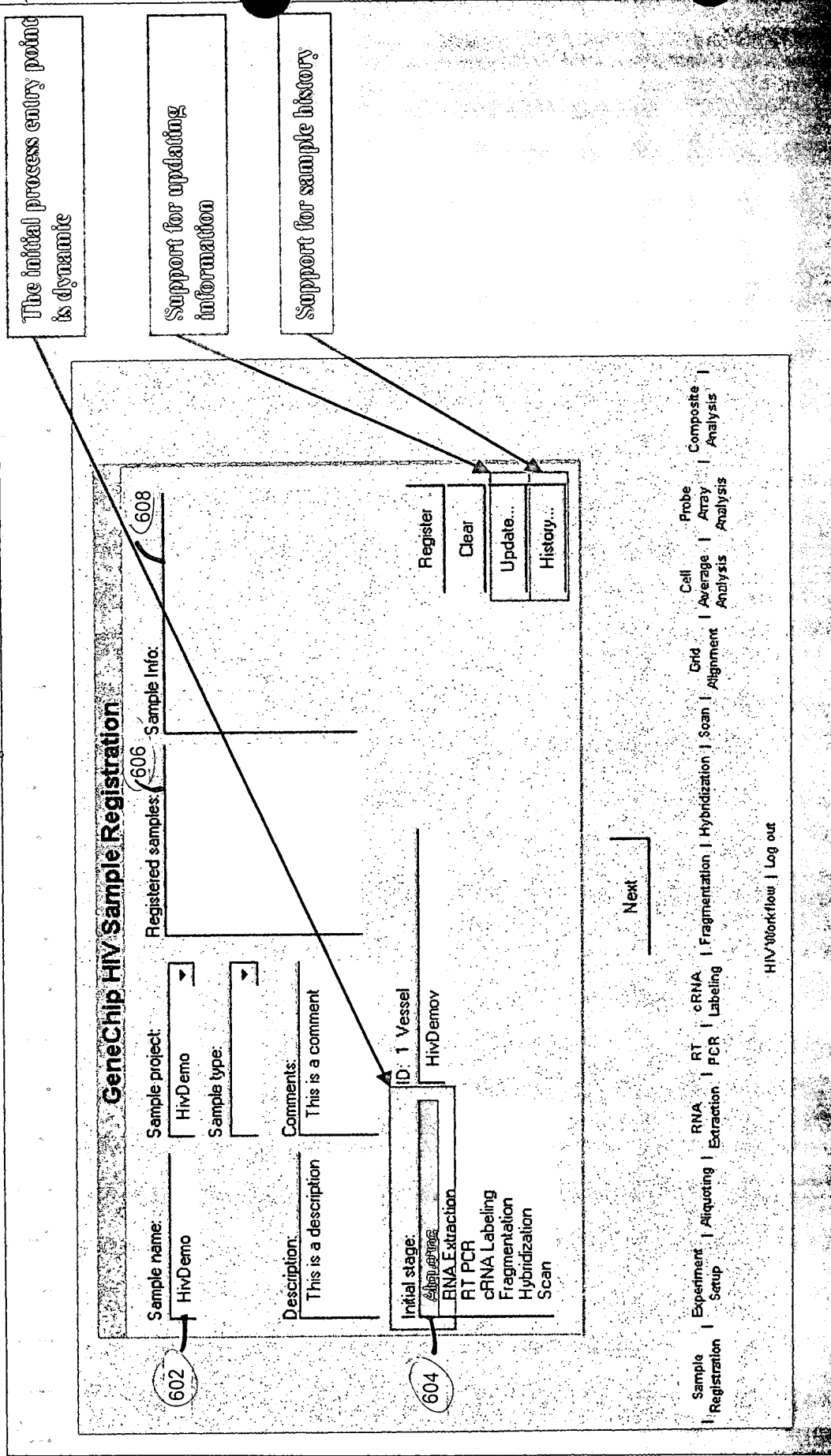


Fig. 6A

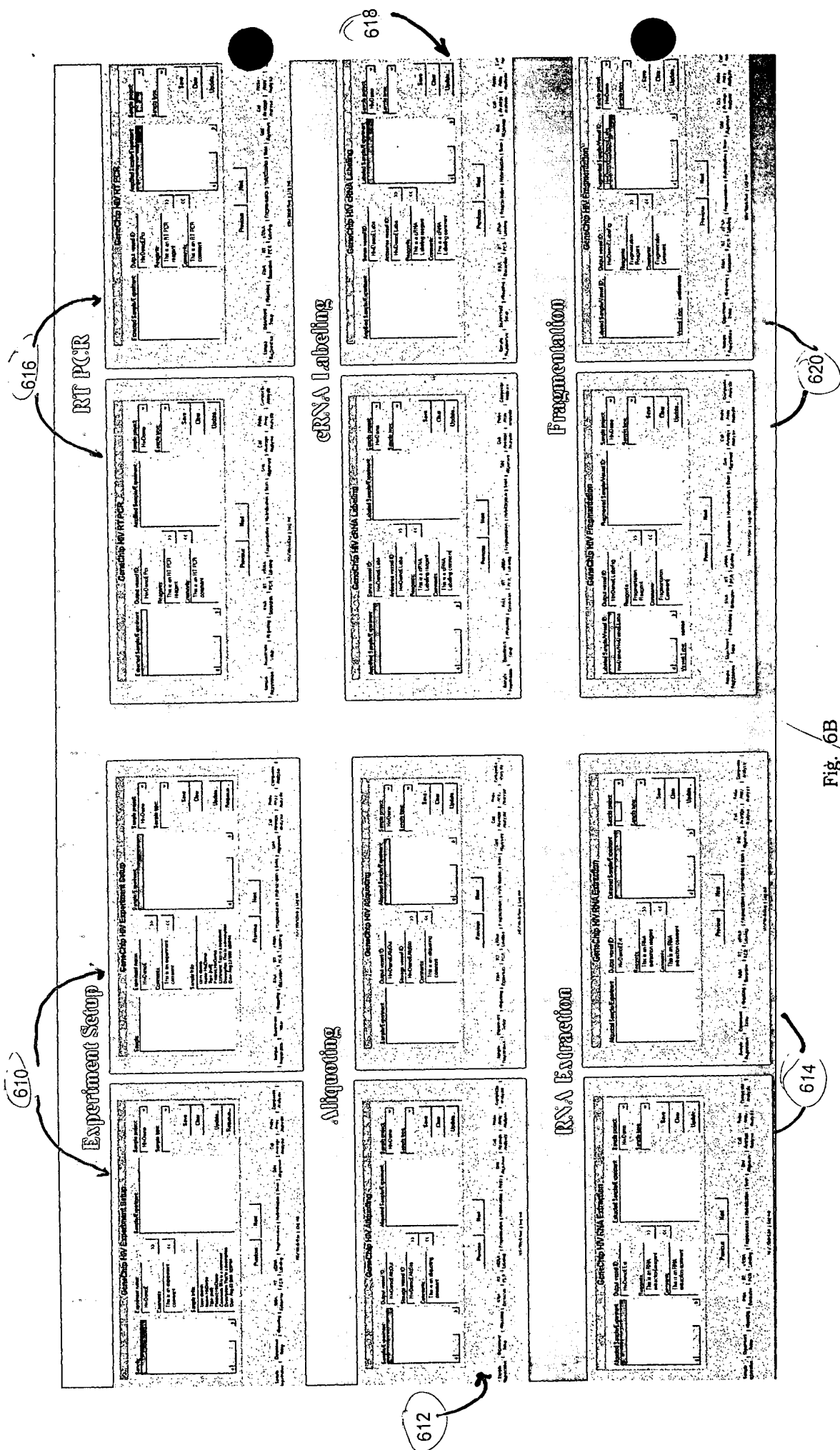


Fig. 6B

Completed hybridization

521

Sample Registration	Experiment Setup	Aliquoting	RNA Extraction	RT-PCR	qRNA Labeling	Fragmentation	Hybridization	Scan	Alignment	Grid	Average Analysis	Cell
---------------------	------------------	------------	----------------	--------	---------------	---------------	---------------	------	-----------	------	------------------	------

65760" 4642660

631

GeneChip HIV Grid Alignment

The grid was manually aligned and sent to cell averaging

Failed automatic grid alignment and is waiting on the queue

Pending GridAlignment

Experiment(s)/Probe Array(s)

632

636

634

Completed GridAlignment

Experiment(s)/Probe Array(s)

Sample Info:
Name - HivDemo
Project - HivDemo
Type - (null)
User - dbernh
Date - Aug 23 1998 128PM
Experiment Info:
Name - HivDemoE

File Type Info:

Probe Array Image ID:
HivDemoCs
File Type: DAT
Name: HivDemoCs.DAT
User/Creator: dbernh
Date/Date: Aug 24 1998

Probe Array Info:

Array Name: HivDemoCs
Array Type: PRT 440S
Lot/Number: Lot # 12345

Sample projects:

HivDemo

Sample types:

Probe array types:

PRT 440S

Grid Alignment:

Manual

Clear

Previous

Next

Sample Registration | Experiment Setup | Aliquoting | RNA Extraction | RT-PCR | cRNA Fragmentation | Hybridization | Sczn | Grid Alignment | Probe Analysis | Composite Analysis

HIV Workflow | Log out

Fig. 6D

GenoChip HIV Cell Average Analysis

Sample projects:

Experiment names:

Sample types:

Probe array types:

User names:

Cell Average Name:

Image Data/Probe Array Type:

Image Data Cell Data:

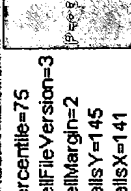
Algorithm:

Parameter:

Run

>>
<<

Results

Image Name	Cell Name	Probe Array Type	Parameters	Result ()
HivDemoCs.DAT	HivdemoCs cel prt 44Ds		Percentile=75 CellFileVersion=3 CellMargin=2 CellsY=145 CellsX=141	

Previous
Next

Sample Registration

Experiment Setup

Aliquoting

RNA Extraction

RT-PCR

cRNA Labeling

Fragmentation

Hybridization

Scan

Grid Alignment

Cell Average Analysis

Probe Array Analysis

Composite Analysis

HIV Workflow | Log out

Fig. 6E

GeneChip HIV Probe Array Analysis

Sample projects:

Experiment names:

Sample types:

Probe array types:

User names:

Probe Array Data:

Cell Data/Probe Array Type:

Probe Array Name:

Algorithm:

GeneChip Rules:

Parameters:

Run:

Clear:

Details:

>> <<

Results

Cell Name	Probe Array Name	Probe Array Type	Parameters	Result (/Fail)
HivDemoCa.CEL	hivdemoca.chp	prt 440a	Ratio=1.2 BOCutoff=15.0 BGSub=-1.0 IntraChipComposite=1	PASS
hivdemocs.cel	hivdemocs.chp	prt 440s	Ratio=1.2 BOCutoff=20.0 BGSub=-1.0 IntraChipComposite=1	PASS

Previous Next

Sample Registration | Experiment Setup | Aliquoting | RNA Extraction | RT-PCR | cRNA Labeling | Fragmentation | Hybridization | Scan | Grid Alignment | Cell Average Analysis | Probe Array Analysis | Composite Analysis

HIV workflow | Log out

GeneChip HIV Composite Analysis

Sample projects:

HivDemo

Experiment names:

HivDemoE

Sample types:

User names:

dberrh

Sense/Antisense Probe Array

Composite Name:

Composite Data:

Algorithm:

GeneChip Rules

Parameter:

Normally

Run

Clear

Defaults

Results

Sense Chip File Name: hivdemoE omp
Antisense Chip File Name: hivdemoE omp
Composite File Name: hivdemoE omp
Parameters: Result (Page)

Previous

Sample Registration | Experiment Setup | Aliquoting | RNA Extraction | RT-PCR | cRNA Labeling | Fragmentation | Hybridization | Scan | Grid Alignment | Coll. Average Analysis | Probe Array Analysis | Composite Analysis

HIV Workflow | Log out

Sample name: HivDemo

EXPERIMENT NAMES WITH COMPLETED PROCESSES:

- HivDemoE
- *Sample Registration
- *Experiment Setup
- *Aliquoting
- *RNA Extraction
- *RT-PCR
- *cRNA Labeling
- *Fragmentation
- *Hybridization**
- *Scan
- <HivDemoCa.DAT
- <HivDemoCs.DAT
- *Grid Alignment
- >HivDemoCa.DAT
- >HivDemoCs.DAT
- *Cell Average Analysis
- <HivDemoCa.CEL

HivDemoE / Hybridization

> Vessel

- *ID: HivDemoELabsFig
- > Probe array
- *ID: HivDemoCs
- *Array type: PRT 440S
- *Lot #: Lot # 12345
- <Hyb Description 0
- *Date: Aug 24 1998 7:12:16AM
- *Name: PRT 440s
- *Reagents: Hiv sense reagent
- *Lot #: Lot #6789
- *Comments: Hiv sense Hyb comment
- *Description: (none)
- *Stages: Completed
- *Station ID: 0
- *Station #: 1
- *Module: 1

Print Preview...

Clear

Cancel

Sample Registration

Experiment Setup

Aliquoting

RNA Extraction

RT-PCR

cRNA Labeling

Fragmentation

Hybridization

Scan

Grid Alignment

Probe Array Analysis

Cell Average Analysis

Composite Analysis

HIV Workflow

Log out

Fig. 6H

[illegible]

701

Probe array types: Hu6800subA 710

User names: dbernh 712

Algorithm: GeneChip Histogram 714

☐ Use set name in analysis

Cell Average Name: 716

Parameter: Percentile=75
CellFileVersion=3
CellMargin=2 718

Existing set name(s): 711

Create/Update set name: 713

Buttons: Run Clear Defaults Create Set...

Image Name	Cell Name	Probe Array Type	Algorithm	Set Name	Result (%)
dbSubA0.dat	dbsuba0.cel	Hu6800subA	GeneChip Percentile	DerekDP0	
dbSubA1.dat	dbsuba1.cel	Hu6800subA	GeneChip Percentile	DerekDP0	
dbSubA10.dat	dbsuba10.cel	Hu6800subA	GeneChip Percentile	DerekDP0	
dbSubA11.dat	dbsuba11.cel	Hu6800subA	GeneChip Percentile	DerekDP1	
dbSubA12.dat	dbsuba12.cel	Hu6800subA	GeneChip Percentile	DerekDP1	
dbSubA13.dat	dbsuba13.cel	Hu6800subA	GeneChip Percentile	DerekDP1	

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Fig. 7A

Assay type

Data type

Probe array type

Month / Day / Year

Sample project

Experiment name

Sample type

User name

GeneChip Expression Cell Data Analysis

Go back to GeneChip Data Analysis Filter page.

Sample projects: ExpMig

Experiment names: dbSubA1

Sample types: ExpMig

Probe array types: Hu6800subA

User names: dbenth

Cell Data/Probe Array Type: Cell Data/Probe Array Type

Probe Array Name: dbsuba1.chp

Algorithm: Robust Multi-array Average (RMA)

Cell Data/Probe Array Name:

Scaling | Normalization | ProbeMask | Baseline | Parameters

SDT Multiplier: 35.00 Modify

Horizontal Zones=4

Vertical Zones=4

%BG Cells=80

STP=3.00

Ratio Threshold=1.50

Ratio Limit=10.00

Abs Pos/Neg Min=3.00

Abs Pos/Neg Max=4.00

☐ Use set name in analysis

Existing set name(s):

Create/Update set name:

Create Set...

Run Clear Defaults

Fig. 7C

Filter to select desired analyses

Project 812	Probe Array 814	Sample Type 816	Operator 818	Sample Name 820	Experiment 822	Analysis 824
AlfyDemo2 AlfyDemo1	1165aa74 1165ba74 1165ca74 1165da74	Liver Lung	dshuld	Alfy Alfy2	rep1basea rep1baseb rep1basec rep1based rep1samp1a rep1samp1b rep1samp1c rep1samp1d rep1samp2a	rep1basea rep1baseb rep1basec rep1based rep1samp1a rep1samp1b rep1samp1c rep1samp1d rep1samp2a

Filter results

Diff Call	Probe Set Name	Avg Diff	Abs Call	Positive	Negative	Pairs Used	Pairs InAvd	Lod	Avd	PM	Excess	MM	Inc	Dec	Ratio	Dec Ra
Sort:		Descending														
Line 1:		>20														
Line 2:		=P														

Build Avg Diff Filter

>20

OK Cancel

Undo

Fig. 8B

665T60"454/6660

Experiment results table

Query results table

Pivot results table

		rep1basea		rep1samp1a	
Project		AlfyDemo1		AlfyDemo1	
Probe Array		1165aa74		1165aa74	
Sample Type		Lung		Lung	
Operator		dshuld		dshuld	
AUG					
Analysis Name	Probe Set Name	Avg Diff	Log Avg	Abs Call	
1 rep1basea	18D00173	2.3	0.16	A	
2 rep1basea	17D00265	75.5	5.19	P	
3 rep1basea	16D10656	7.2	0.51	A	
4 rep1basea	13D10704	37.0	0.90	A	
AUG					
		rep1basea		rep1samp1a	
		Avg Diff	Abs Call	Avg Diff	Abs Call
18D00173		2.3	A	0.9	A
17D00265		75.5	P	66.5	P
16D10656		7.2	A	0.4	A
13D10704		37.0	A	26.8	A
158D10924		2.6	A	3.6	A
1429D11139		4.2	A	0.2	A
101D12620		2.8	A	4.8	A
109D13138		14.5	A	29.1	P
103D13315_1		129.2	P	216.9	P
1315D13639		120.2	P	90.9	P
108D13665		8.4	A	1.6	A
AUG					
Experiment Info		Query	Pivot		

Fig. 8C

65T60"4644660

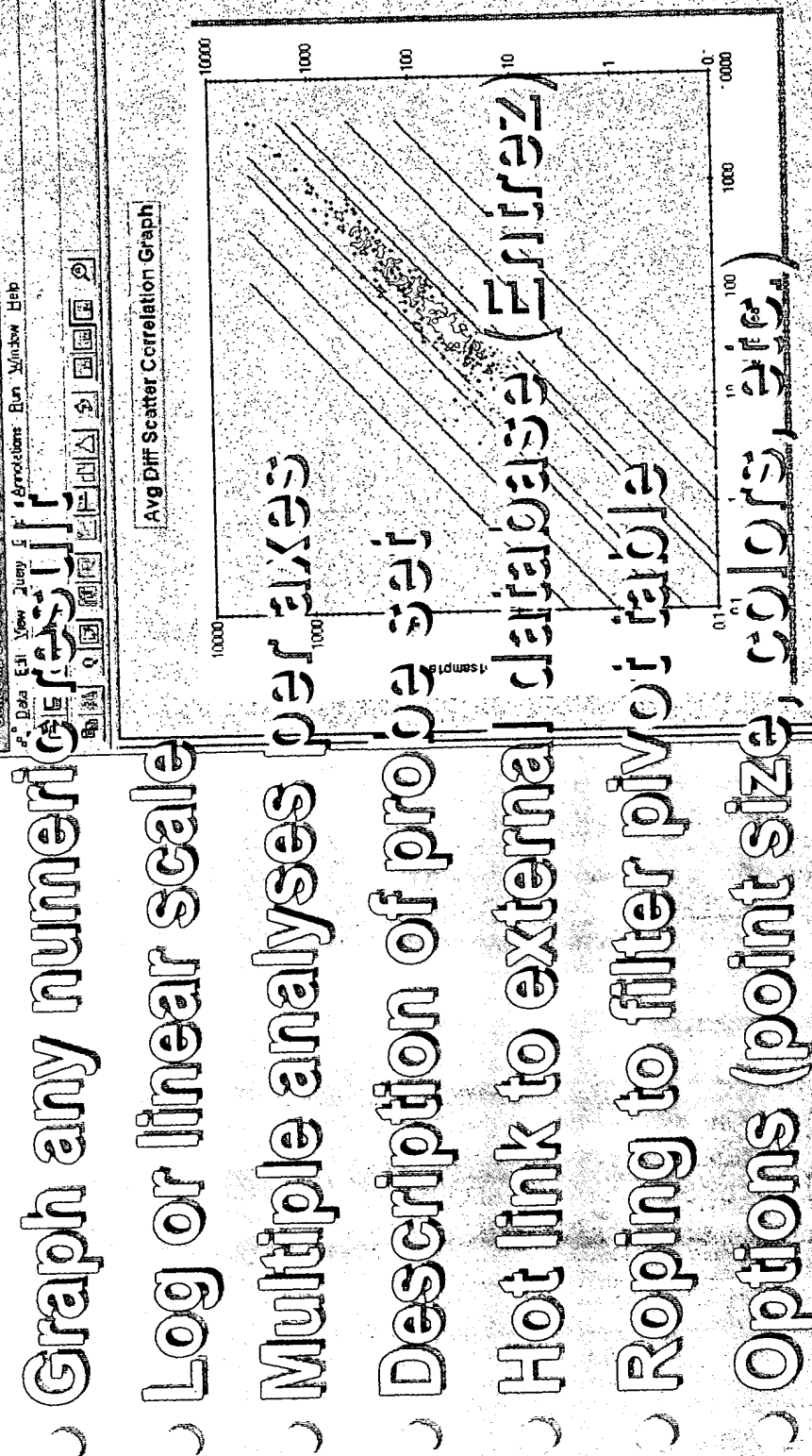


Fig. 8D

Recompute fold change

Log or linear scale

Description of probe set

Hot link to external database (Entrez)

Linking to filter pivot table

Options (point size, colors, etc.)

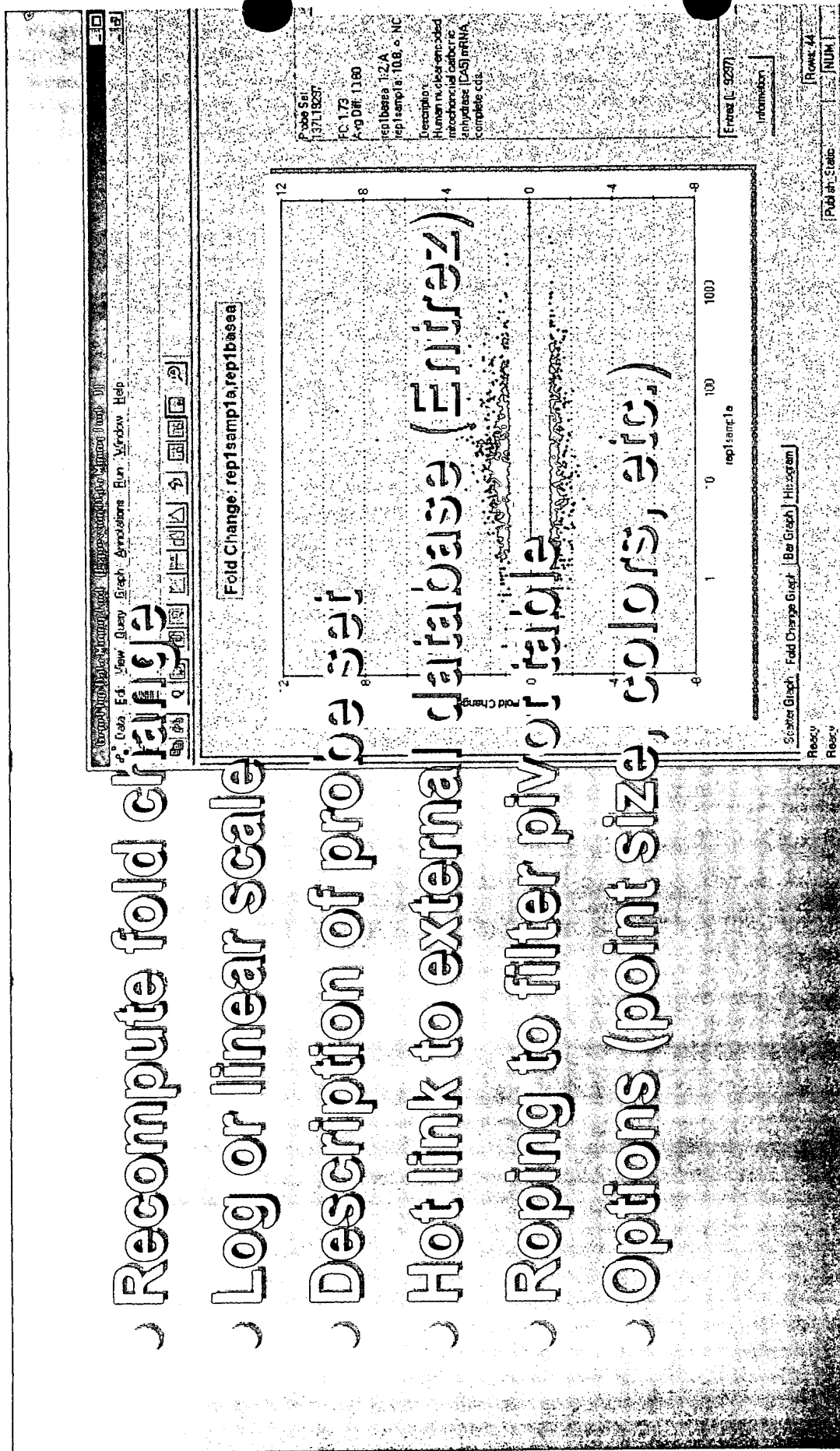


Fig. 8E

665T60"46426660

- Graph any numerical results
- Options (bar size, colors, size)

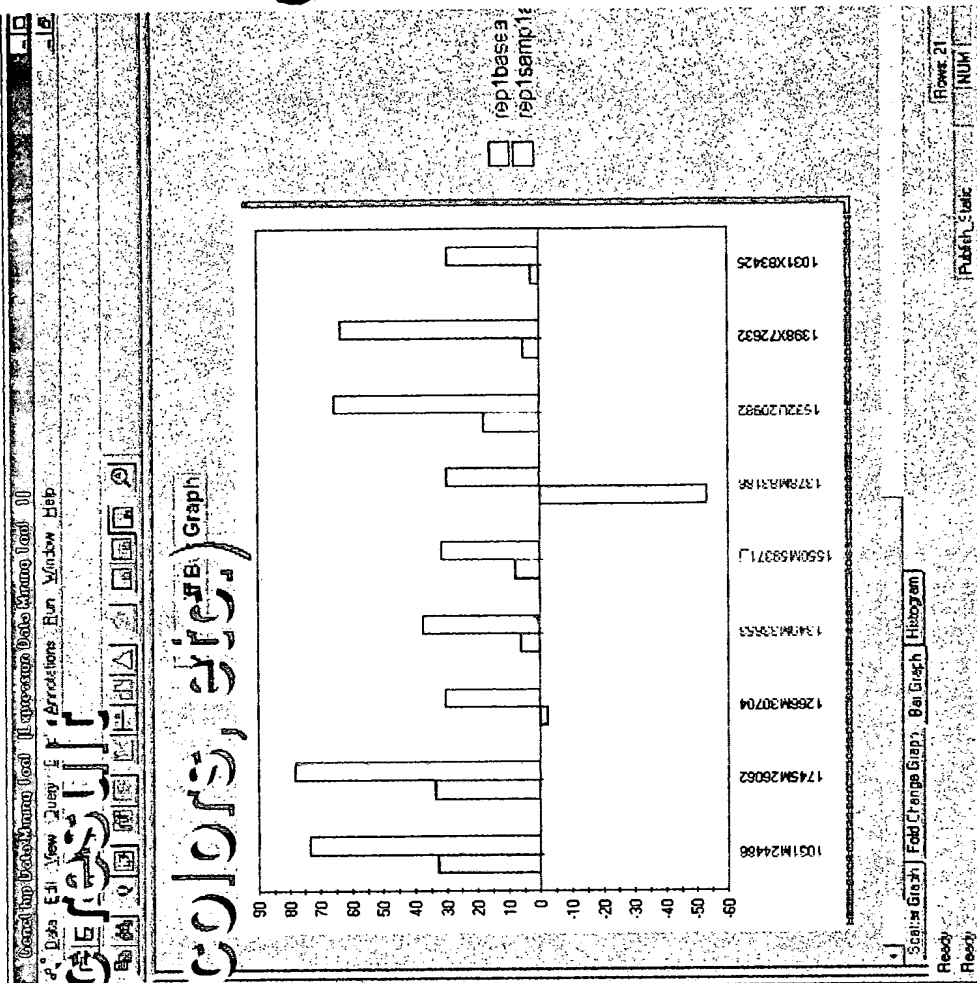


Fig. 8F

Histogram Graph

- Histogram of average difference
- Landmarks
- Options (bin size, range, colors, etc.)

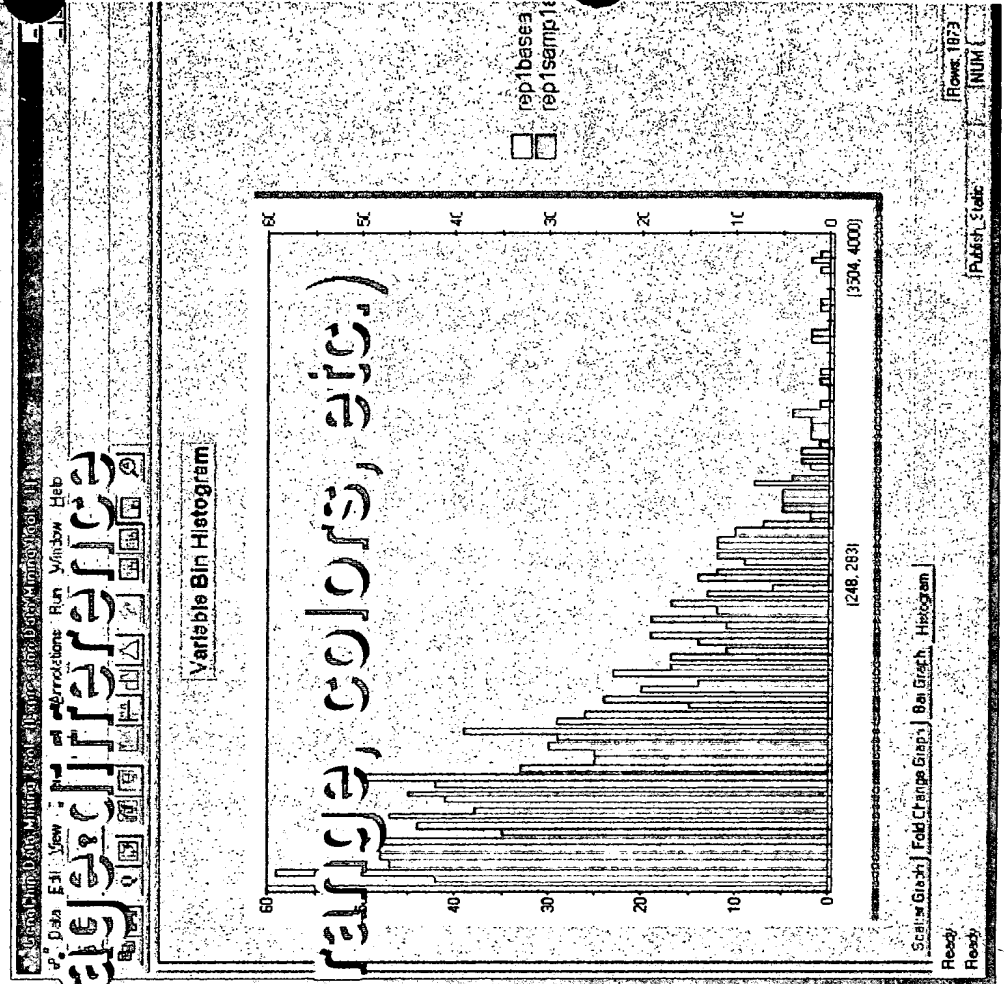


Fig. 8G

US 2002/0164660 A1

Filters saved to DataMiningInfo database Name saved queries

Save

foo	NewlySavedQuery	show
Highly expressed genes	NewlySavedQuery2	t1
lcl1	one	t11
l1	query	t2
l1 test	read-only	t22
l1	read-only2	t23
My favorite query	ro	t3
network	save1	test1
new	scatter	test2

Name: _____

☐ Only show my queries.
☐ Show save changes dialog.

Save Cancel

Fig. 9A

Annotate probe set(s)

Annotations include

- Annotation text
- Type (user defined)
- User name
- Date of annotation

Annotate

Probe Set(s): 109D13138

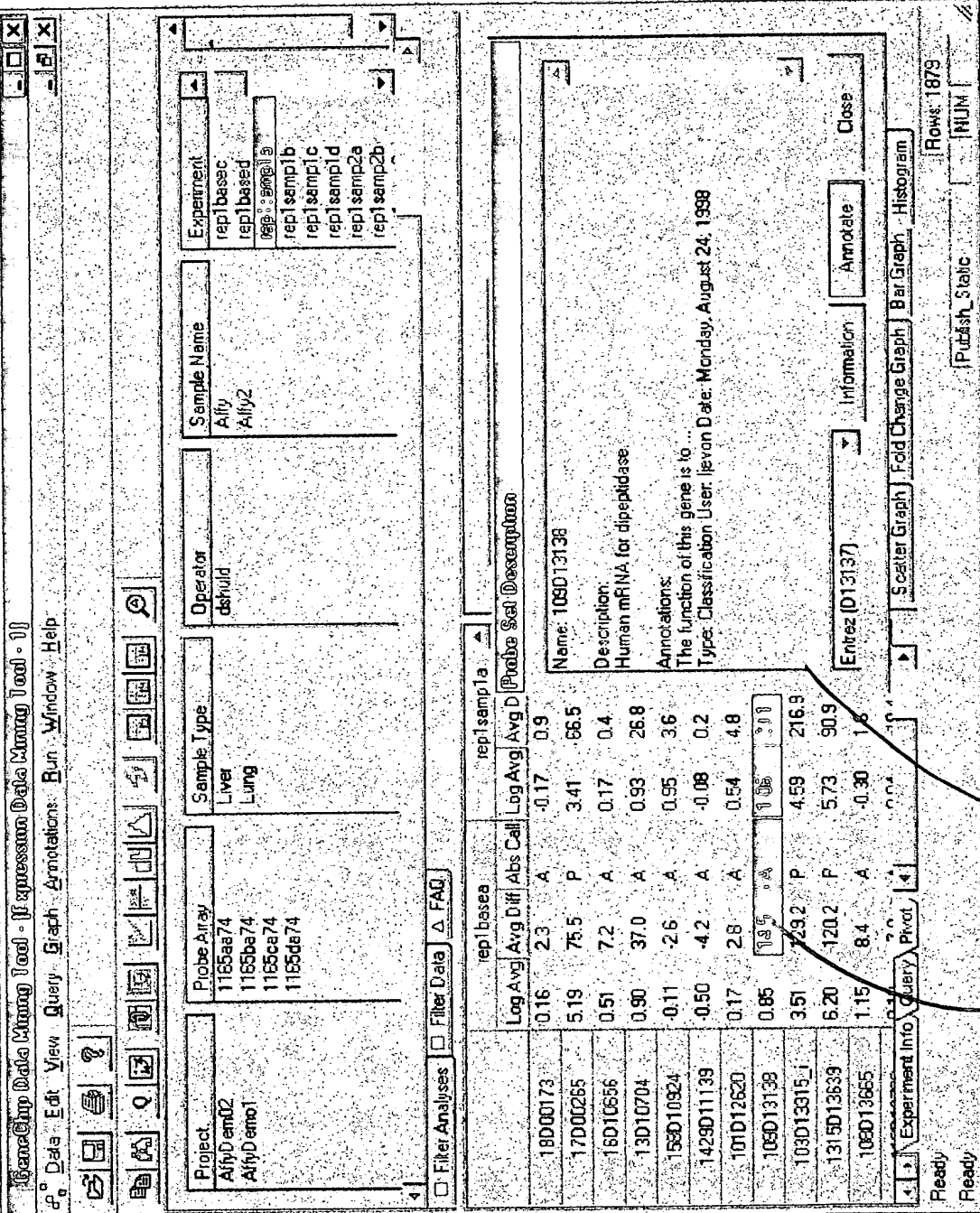
Annotation Type: Classification

Annotation: The function of this gene is to...

OK Cancel

903

Fig. 9B



Specify multiple constraints (filters)
Update annotations (owner only)

910

Query Annotations					
Field	Search For	Operation	User	Date	Description
Probe Set	109D	AND			
Classification	function	AND			
>>					
Probe Set	Type	Annotation	User	Date	Description
1	109D13138	Classification		8/24/99 4:02:21 PM	Human mRNA for dipeptidase

Fig. 9D

Provided by Chip Design

912

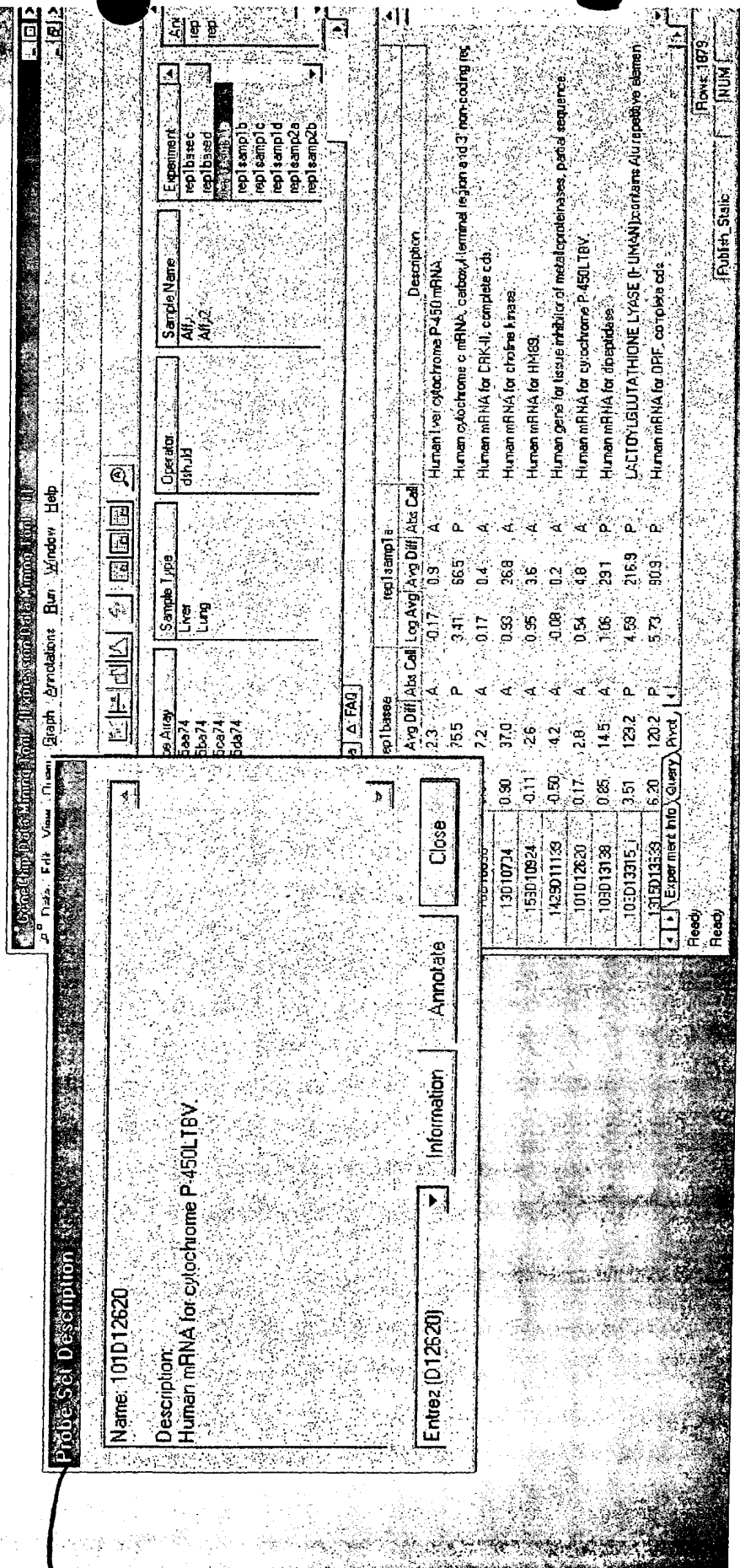


Fig. 9E

Search the descriptions database

User defines search criteria

Results added to filter

Search Array Descriptions		
Search for:		
Human AND receptor AND kinase		
Probe Set	Array Type(s)	Description
24013168	1165aa74	Human gene for endothelin-B receptor (hET-BR).
506D15056	1165da74	Human gene for thromboxane A2 receptor, exon
106D16532	1165aa74	Human gene for very low density lipoprotein rece
301U18934.1	1165ca74	Human receptor tyrosine kinase (DTK) mRNA, cc
1745M74782	1165aa74	INTERLEUKIN-3 RECEPTOR ALPHA CHAIN PT
1477L20859	1165aa74	Human leukemia virus receptor 1 (GLVR1) mRNA
1263M69238	1165aa74	Human aryl hydrocarbon receptor nuclear transi
203D13305	1165ba74	Human mRNA for brain cholecystokinin receptor
170D25235	1165aa74	Human mRNA for alpha1C adrenergic receptor, c
170M15288	1165aa74	Human G-protein-coupled receptor kinase 10 (GRK
4		

Fig. 96

Probe Set Description

Name: 109D13138

Description:
Human mRNA for dipeptidase.

Annotations:
The function of this gene is to
Type: Classification User: Revision Date: Monday, August 24, 1998

Entrez (D13137) Information Annotate Close

Probe Set Description dialog

Browser Window

GenBank Data Entry Tool (Internet Browser)

Data Edit View Window Help

Back Forward Stop Refresh LMS

NCBI Entrez Nucleotide Query ELAST Entrez ?

Other Formats: FASTA Graphic

LOCUS HUMDP10 380 bp DNA PRI 03-APR-1993

DEFINITION Human dipeptidase gene, exon 1C.

ACCESSION D13137

KEYWORDS dipeptidase.

SOURCE Homo sapiens liver DNA, clone lib:genomic library.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 380)

AUTHORS Satch, S., Kusumaki, C., Kenta, Y., Niva, E. and Kohsaka, X.

TITLE Cloning and structural analysis of genomic DNA for human renal dipeptidase

JOURNAL Biochim. Biophys. Acta 1172 (1-2), 18-183 (1993)

MEDLINE 93176806

REFERENCE 2 (bases 1 to 380)

AUTHORS Satch, S.

TITLE Direct Submission

JOURNAL Submitted (01-SEP-1992) to the DDBJ/EMBL/GenBank databases. Subura

For Help, press F1

NUM

Fig. 10A

FAQ's

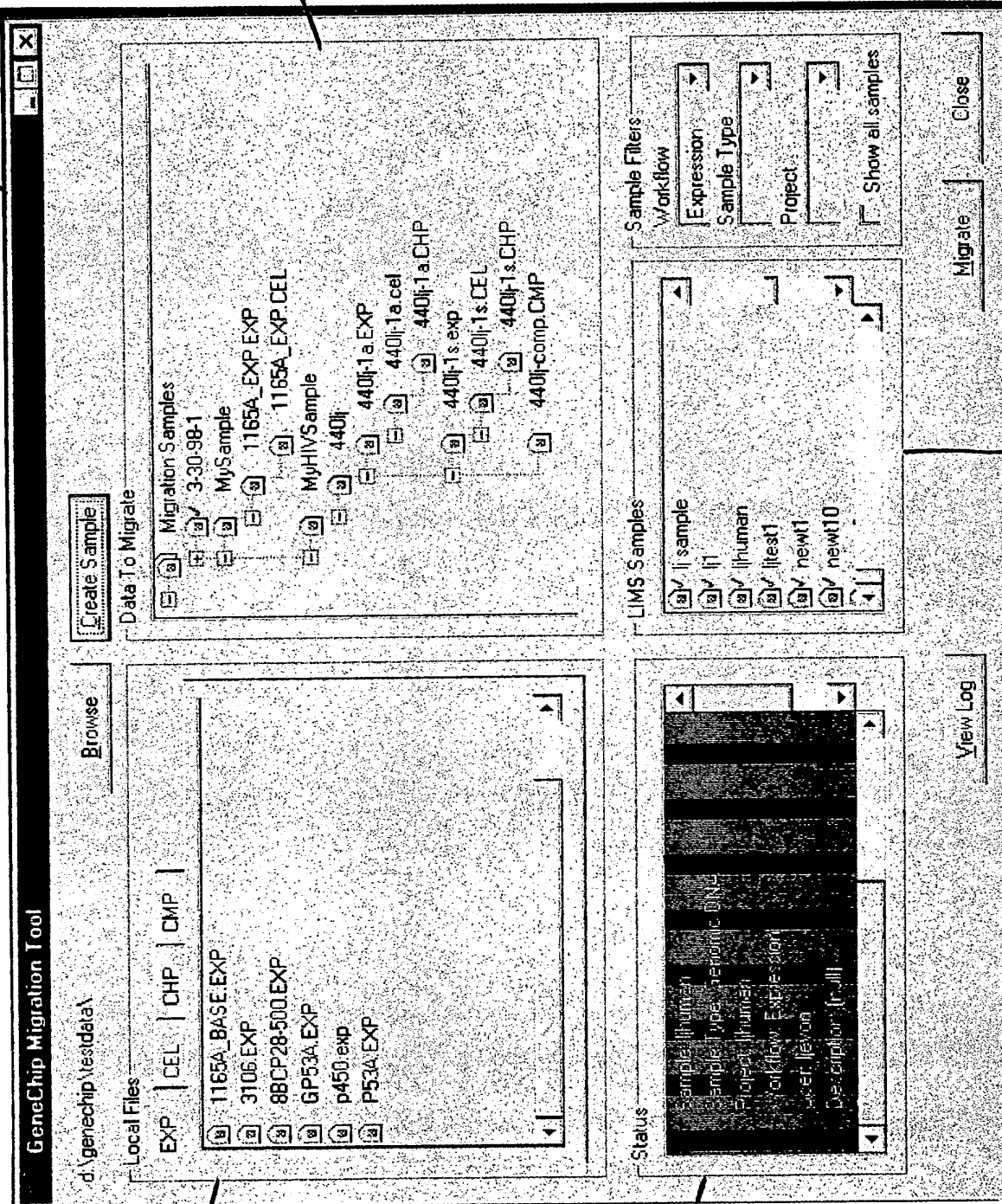
increase in average difference intensity (I_{av}) in the

Questions

Results

[illegible]

Fig. 10B



1024

1028

1026

1030

Fig. 10C

665760"464/5E60

1031

Fluores Station 1

#	Experiment Name	Probe Array Type	Protocol	Current Stage	Time/Cycle	Temp	Close
1	1165A_BASE	1165ARA	EMGEWS1				Run
2	[No Probe Array]						
3	[No Probe Array]						
4	[No Probe Array]						

Fluores Station 1

Assay Types: Expression Experiments: Probe Array Types: Protocols: EMGEWS1

Vessel Bar Code: TEADTSE Probe Array Lot: 71449 Hybridized Experiments: 000Ahigh

Sample Projects: [All Projects] Reagents: Reagent Lot: 710812-04

Users: jlevon Comments: 15nov/97

Hybridization Run

Experiment: Probe Array Type: Protocol: Time/Cycle: Temp: Run

Clear Refresh Close

File Mode

LIMS Mode

Fig. 10D

1041 COSTED "1942425E50"

Scanner

Experiment Name: 1165A_BASE

Probe Array Type: 1165ARA

Data File Location: d:\genetechip\testdata

Number of Scans: 4

Scanned Experiments: 1165A_BASE, 1165A_EXP, p450, P53A

Start Options... Laser ON Cancel

File Mode

Scanner

Assay Types: Expression

Experiments: lhuman_a2, lhuman_a3, lhuman_a4

Sample Projects: [All Projects]

Users: ljevon

Probe Array Image ID: 000Ahigh

Comments: 15nov97

Probe Array Type: 1228a71a

Number of Scans: 1

Data File Location: \\DBSERVER02\GCLIMS\data

Start Options... Laser ON Cancel

LIMS Mode

Fig. 10E

1051
1052

Experiment Information	
Data File Location:	d:\genchip\testdata
Experiment Name:	P53A
Current Experiments:	<div> <div>3106</div> <div>440lj_1a</div> <div>440lj_1s</div> <div>88CP28-500</div> </div>
Scanned Experiments:	<div> <div>1165A_BASE</div> <div>1165A_EXP</div> <div>p450</div> <div>P53A</div> </div>
Probe Array Type:	GP53
Probe Array Lot:	601500.6#516
Operator Name:	JHC
Sample Type:	DNA
Sample Description:	Flourescein
Sample Project:	p53
Comments:	
Reagents:	3x
Reagent Lot:	
<div> <div>Save</div> <div>Clear</div> <div>Edit</div> <div>Print</div> <div>Delete</div> </div>	
<div> <div>Next ></div> <div>< Back</div> <div>Close</div> </div>	

File Mode

Experiment Information	
Data File Location:	\\DBSERVER02\GCLIMS\Data
Experiment Name:	000Ahigh
Current Experiments:	<div> <div>ihuman_a2</div> <div>ihuman_a3</div> <div>ihuman_a4</div> <div>ip53c</div> </div>
Scanned Experiments:	<div> <div>000Ahigh</div> <div>000Bhigh</div> <div>000Chigh</div> <div>000Dhigh</div> </div>
Assay Types:	[All Types]
Sample Projects:	[All Projects]
Users:	lievon
Probe Array Type:	1228a71a
Probe Array Lot:	71449
Operator Name:	lievon
Sample Type:	cDNA, ds
Sample Description:	
Sample Project:	Yeast
Comments:	[null]
Reagents:	
Reagent Lot:	710812.04
<div> <div>View</div> <div>Print</div> <div>< Back</div> <div>Next ></div> <div>Close</div> </div>	

LIMS Mode

Fig. 10F